

Table 1. General characteristics of the analysed chromosomes.

chromosome	abbr.	taxonomy	A	dna A	C	co- loc.	note	G	L	obs.	exp.	obs/exp	p
<i>Agrobacterium tumefaciens</i> C58 Cereon circular chr I.	ag t	α Proteobacteria	+	1	+	ab		-	-	325	331	0.98	0.414
<i>Agrobacterium tumefaciens</i> C58 Cereon linear chr II.			+	0	-	O		-	-	219	243	0.90	0.131
<i>Aquifex aeolicus</i> VF5	aq a	Aquificales	-	1	+	(abd)	local extreme; shift of dnaA	-	-	485	439	1.10	0.065
<i>Bacillus anthracis</i> Ames	ba a	Firmicutes, Bacilli	+	1	+	abd		+	+	1673	1813	0.92	0.009
<i>Bacillus cereus</i> ATCC14579	ba c	Firmicutes, Bacilli	+	1	+	abd		+	+	1627	1879	0.87	1.0E-05
<i>Bacillus halodurans</i>	ba h	Firmicutes, Bacilli	+	1	+	abd		-	+	1147	1181	0.97	0.243
<i>Bacillus subtilis</i> 168	ba s	Firmicutes, Bacilli	+	1	+	abd		+	+	1124	1191	0.94	0.082
<i>Bacteroides thetaiotaomicron</i> VPI-5482	bc t	Bacteroidetes/Chlorobi group	+	1	+	(ab)	shift of extreme and boxes	-	-	2198	1811	1.21	4.7E-10
<i>Bdellovibrio bacteriovorus</i> HD100	bl b	δ Proteobacteria	+	1	+	a(b)d)	shift of boxes	-	-	915	781	1.17	0.0006
<i>Bifidobacterium longum</i> NCC2705	bi l	Actinobacteria	-	1	+	(a)bd)	shift of local extreme	-	+	355	247	1.44	5.5E-06
<i>Blochmannia floridanus</i>	bl f	γ Proteobacteria	+	0	-	O		-	-	270	253	1.07	0.230
<i>Bordetella bronchiseptica</i> RB50	bo br	β Proteobacteria	+	1	+	abd		-	-	279	268	1.04	0.311
<i>Bordetella parapertussis</i> 12822	bo pa	β Proteobacteria	+	1	+	abd		-	-	251	239	1.05	0.286
<i>Bordetella pertussis</i> Tohama I	bo pe	β Proteobacteria	+	1	+	(ab)	local extreme	-	-	214	213	1.00	0.487
<i>Borrelia burgdorferi</i> B31	be b	Spirochaetales	+	1	-	ad		-	-	265	328	0.81	0.005
<i>Bradyrhizobium japonicum</i> USDA110	bd j	α Proteobacteria	+	1	-	(ad)	shift of extreme and dnaA	-	-	376	700	0.54	2.3E-23
<i>Brucella melitensis</i> 16M chr. I	br m	α Proteobacteria	+	1	+	ab(d)	shift of dnaA	-	-	326	291	1.12	0.081
<i>Brucella melitensis</i> 16M chr. II			+	0	-	(ab)	two boxes	-	-	161	160	1.01	0.477
<i>Brucella suis</i> 1330 chr. I			+	1	+	ab(d)	shift of dnaA	-	-	321	289	1.11	0.097
<i>Brucella suis</i> 1330 chr. II	br s	α Proteobacteria	+	0	-	(abd)	two boxes; agreement with <i>repC</i>	-	-	174	164	1.06	0.298
<i>Buchnera aphidicola</i> APS	bu a	γ Proteobacteria	+	1	-	(abd)	two boxes; shifts	-	-	148	227	0.65	2.3E-05
<i>Campylobacter jejuni</i> NCTC11168	ca j	ε Proteobacteria	+	1	+	ad		-	-	728	593	1.23	1.0E-04
<i>Caulobacter crescentus</i> CB15	ca c	α Proteobacteria	+	1	-	ad		-	-	157	222	0.71	4.1E-04
<i>Chlamydia muridarum</i>	ch m	Chlamydiales	+	2	+	O		-	-	392	335	1.17	0.017
<i>Chlamydia trachomatis</i>	ch t	Chlamydiales	+	2	+	O		-	-	401	317	1.27	0.001
<i>Chlamydophila caviae</i> GPIC	ch c	Chlamydiales	+	2	+	O		-	-	469	377	1.24	0.001

<i>Chlamydophila pneumoniae</i> CWL029	ch p	Chlamydiales	+	2	+	(bd)	coincidental agreement, not present in other chlamydia	-	-	380	381	1.00	0.480
<i>Chlorobium tepidum</i> TLS	cb t	Bacteroidetes/Chlorobi group	+	1	+	(abd)	plateau of extreme	-	+	298	310	0.96	0.312
<i>Chromobacterium violaceum</i> ATCC12472	cr v	β Proteobacteria	+	1	+	ab(d)	shift of dnaA	+	-	393	338	1.16	0.022
<i>Clostridium acetobutylicum</i> ATCC824	cl a	Firmicutes, Clostridia	+	1	+	abd		+	+	1754	1423	1.23	2.1E-09
<i>Clostridium perfringens</i> 13	cl p	Firmicutes, Clostridia	+	1	+	abd		+	+	1154	1094	1.06	0.101
<i>Clostridium tetani</i> E88	cl t	Firmicutes, Clostridia	+	1	+	abd		+	+	1263	1011	1.25	5.9E-08
<i>Corynebacterium diphtheriae</i> NCTC13129	co d	Actinobacteria	+	1	+	abd		+	+	627	437	1.43	3E-09
<i>Corynebacterium efficiens</i> YS-314	co e	Actinobacteria	+	1	+	(abd)	shift of extreme	+	+	551	264	2.08	5.1E-24
<i>Corynebacterium glutamicum</i> ATCC13032	co g	Actinobacteria	+	1	+	abd		+	+	890	570	1.56	2.6E-17
<i>Coxiella burnetii</i> RSA493	cx b	γ Proteobacteria	+	1	+	(ad)	shift of extreme and dnaA	-	-	714	581	1.23	1.0E-04
<i>Deinococcus radiodurans</i> R1 chr. I	de r	Thermus/Deinococcus group	+	1	+	(abd)	shift of local extreme	-	+	139	150	0.93	0.263
<i>Deinococcus radiodurans</i> R1 chr. II			-	0	-	O		-	-	30	24	1.24	0.213
<i>Enterococcus faecalis</i> V583	en f	Firmicutes, Bacilli	+	1	+	abd		+	+	1194	1074	1.11	0.006
<i>Escherichia coli</i> K12	e cK	γ Proteobacteria	+	1	+	abd		+	-	1344	951	1.41	1.1E-16
<i>Escherichia coli</i> O157:H7 RIMD0509952	e cO	γ Proteobacteria	+	1	+	abd		+	-	1637	1142	1.43	3.1E-21
<i>Fusobacterium nucleatum</i> ATCC25586	fu n	Fusobacteriales	+	1	+	a(b)d)	shift of boxes	-	-	905	778	1.16	0.001
<i>Geobacter sulfurreducens</i> PCA	ge s	δ Proteobacteria	+	1	+	ab		-	-	406	390	1.04	0.2861
<i>Gloeobacter violaceus</i> PCC7421	gl v	Cyanobacteria	-	1	-	(ad)	local extreme	-	-	514	434	1.18	0.005
<i>Haemophilus ducreyi</i> 35000HP	ha d	γ Proteobacteria	+	1	+	ab		-	-	745	560	1.33	1.4E-07
<i>Haemophilus influenzae</i> Rd KW20	ha i	γ Proteobacteria	+	1	+	O		-	-	845	603	1.40	9.8E-11
<i>Helicobacter hepaticus</i> ATCC51449	he h	ε Proteobacteria	+	1	+	(ad)	shift of extreme and dnaA	-	-	1046	619	1.69	5.6E-26
<i>Helicobacter pylori</i> 26695	he p	ε Proteobacteria	+	1	+	(ad)	shift of extreme and dnaA	-	-	837	540	1.55	6.5E-16
<i>Helicobacter pylori</i> J99	he pJ	ε Proteobacteria	+	1	+	ad		-	-	820	529	1.55	1.0E-15
<i>Lactobacillus johnsonii</i> NCC533	lb j	Firmicutes, Bacilli	+	1	+	abd		+	+	670	699	0.96	0.2199
<i>Lactobacillus plantarum</i> WCFS1	lb p	Firmicutes, Bacilli	+	1	+	abd		-	+	1049	903	1.16	4.8E-04
<i>Lactococcus lactis</i> IL1403	lc l	Firmicutes, Bacilli	+	1	+	abd		+	+	870	821	1.06	0.116
<i>Leptospira interrogans lai</i> 56601 chr. I	le i	Spirochaetales	+	1	+	ad		-	-	1192	1511	0.79	4.5E-10
<i>Leptospira interrogans lai</i> 56601 chr. II			+	0	-	O		-	-	93	125	0.74	0.015
<i>Listeria innocua</i> Clip11262	li i	Firmicutes, Bacilli	+	1	+	abd		+	+	1066	1007	1.06	0.098
<i>Listeria monocytogenes</i> EGD	li m	Firmicutes, Bacilli	+	1	+	abd		+	+	1089	974	1.12	0.006
<i>Mesorhizobium loti</i> MAFF303099	me l	α Proteobacteria	+	1	-	(bd)	distance between boxes > 100 bp	-	-	413	613	0.67	2.1E-10

<i>Mycobacterium avium paratuberculosis</i> k10	mb a	Actinobacteria	+	1	+	(a)bd	local extreme	-	-	175	209	0.84	0.0415
<i>Mycobacterium bovis</i> AF2122/97	mb b	Actinobacteria	+	1	+	a(b)d	shift of boxes	-	-	302	285	1.06	0.243
<i>Mycobacterium leprae</i> TN	mb l	Actinobacteria	+	1	+	abd		-	-	475	429	1.11	0.064
<i>Mycobacterium tuberculosis</i> H37Rv	mb t	Actinobacteria	+	1	+	a(b)d	shift of boxes	-	-	331	290	1.14	0.050
<i>Mycoplasma gallisepticum</i> R	mp ga	Firmicutes, Mollicutes	+	1	-	ad		-	-	326	359	0.91	0.103
<i>Mycoplasma genitalium</i>	mp ge	Firmicutes, Mollicutes	+	1	+	ad		-	-	189	209	0.91	0.161
<i>Mycoplasma mycoides mycoides</i> SC	mp m	Firmicutes, Mollicutes	+	1	+	bd		-	-	245	413	0.59	3E-11
<i>Mycoplasma penetrans</i>	mp pe	Firmicutes, Mollicutes	+	1	-	ad		-	-	477	478	1.00	0.494
<i>Mycoplasma pneumoniae</i> M129	mp pn	Firmicutes, Mollicutes	+	1	-	ad		-	-	304	257	1.18	0.023
<i>Mycoplasma pulmonis</i> UAB CTIP	mp pu	Firmicutes, Mollicutes	+	1	+	abd		-	-	250	343	0.73	7.2E-05
<i>Neisseria meningitidis</i> MC58 B	n mM	β Proteobacteria	+	1	+	(ab)	shift of extreme and boxes	-	+	577	447	1.29	2.6E-05
<i>Neisseria meningitidis</i> Z2491 A	n mZ	β Proteobacteria	+	1	+	(ab)	shift of extreme and boxes	-	+	546	423	1.29	4.1E-05
<i>Nitrosomonas europaea</i> ATCC19718	ni e	β Proteobacteria	+	1	+	(a)bd	shift of local extreme	-	-	704	579	1.22	2.4E-04
<i>Nostoc</i> sp. PCC7120	no	Cyanobacteria	-	1	+	(a)bd	local extreme	-	-	2372	1945	1.22	3.9E-11
<i>Oceanobacillus iheyensis</i> HTE831	oc i	Firmicutes, Bacilli	+	1	+	abd		-	+	1547	1253	1.23	1.4E-08
<i>Pasteurella multocida</i> PM70	pa m	γ Proteobacteria	+	1	+	ab		-	-	1126	703	1.60	2.5E-23
<i>Photothabdus luminescens laumondii</i> TTO1	ph l	γ Proteobacteria	+	1	+	abd		-	-	2406	1647	1.46	4.0E-33
<i>Phytoplasma asteris</i> OY-M	pt a	Firmicutes, Mollicutes	-	1	-	(ad)	local extreme	-	-	267	309	0.86	0.0407
<i>Pirellula</i> sp. 1	pi	Planctomycetes	+	2	-	O		-	-	468	1111	0.42	3.8E-59
<i>Porphyromonas gingivalis</i> W83	po g	Bacteroidetes/Chlorobi group	+	1	+	ad		-	-	612	545	1.12	0.024
<i>Prochlorococcus marinus</i> CCMP1375	pr m	Cyanobacteria	+	1	+	O		-	-	439	597	0.74	4.8E-07
<i>Pseudomonas aeruginosa</i> PAO1	ps a	γ Proteobacteria	+	1	+	abd		+	+	423	373	1.14	0.037
<i>Pseudomonas putida</i> KT2440	ps p	γ Proteobacteria	+	1	+	abd		+	+	723	601	1.20	4.0E-04
<i>Pseudomonas syringae</i> pv. tomato DC3000	ps s	γ Proteobacteria	+	1	+	abd		+	+	920	803	1.15	0.002
<i>Ralstonia solanacearum</i> GMI1000	ra s	β Proteobacteria	+	1	+	abd		+	-	187	210	0.89	0.128
<i>Rhodopseudomonas palustris</i> CGA009	rh p	α Proteobacteria	+	1	+	(ad)	shift of extreme and dnaA	-	-	210	381	0.55	1E-12
<i>Rickettsia conorii</i> Malish 7	ri c	α Proteobacteria	+	1	+	ab		-	-	356	455	0.78	2.6E-04
<i>Rickettsia prowazekii</i> Madrid E	ri p	α Proteobacteria	+	1	+	ab		-	-	349	401	0.87	0.028
<i>Salmonella enterica</i> Typhi	sa e	γ Proteobacteria	+	1	+	abd		-	-	1449	917	1.58	3.9E-28
<i>Salmonella typhimurium</i> LT2	sa t	γ Proteobacteria	+	1	+	abd		+	-	1439	920	1.56	5.2E-27
<i>Shewanella oneidensis</i> MR-1	sh o	γ Proteobacteria	+	1	+	abd		-	+	1881	1280	1.47	5.1E-27
<i>Shigella flexneri</i> 2a 301	sg f	γ Proteobacteria	+	1	+	a(b)d	not clear cluster of boxes	-	-	1307	939	1.39	4.2E-15

<i>Sinorhizobium meliloti</i> 1021	si m	α Proteobacteria	+	1	+	ab		-	-	198	319	0.62	5.3E-08
<i>Staphylococcus aureus</i> Mu50	st a	Firmicutes, Bacilli	+	1	+	abd		-	+	1118	1028	1.09	0.026
<i>Staphylococcus epidermidis</i> ATCC12228	st e	Firmicutes, Bacilli	+	1	+	abd		+	+	907	898	1.01	0.411
<i>Streptococcus agalactiae</i> 2603V/R	sc a	Firmicutes, Bacilli	+	1	+	abd		-	+	757	746	1.01	0.388
<i>Streptococcus mutans</i> UA159	sc m	Firmicutes, Bacilli	+	1	+	abd		-	+	781	687	1.14	0.007
<i>Streptococcus pneumoniae</i> R6	sc pn	Firmicutes, Bacilli	+	1	+	abd		-	+	876	647	1.35	2.1E-09
<i>Streptococcus pyogenes</i> M1 GAS	sc py	Firmicutes, Bacilli	+	1	+	abd		-	+	729	605	1.20	3.5E-04
<i>Streptomyces avermitilis</i> MA-4680	sm a	Actinobacteria	-	1	+	(a)bd	local extreme	-	-	337	326	1.03	0.334
<i>Streptomyces coelicolor</i> A3(2)	sm c	Actinobacteria	+	1	+	(a)bd	shift of extreme	-	-	235	259	0.91	0.143
<i>Synechococcus</i> sp. WH8102	so	Cyanobacteria	+	1	+	O		-	-	255	282	0.90	0.120
<i>Synechocystis</i> sp. PCC6803	sy	Cyanobacteria	-	1	+	ab		-	-	1171	853	1.37	7.2E-13
<i>Thermoanaerobacter tengcongensis</i> MB4T	ta t	Firmicutes, Clostridia	+	1	+	abd		-	+	1050	897	1.17	2.6E-04
<i>Thermosynechococcus elongatus</i> BP-1	ts e	Cyanobacteria	+	1	+	ab		-	-	652	444	1.47	1.5E-10
<i>Thermotoga maritima</i>	th m	Thermotogales	+	1	-	O		-	-	552	474	1.17	0.007
<i>Treponema denticola</i> ATCC35405	tr d	Spirochaetales	+	1	+	(ab)	shift of extreme and boxes	-	-	830	942	0.88	0.0038
<i>Treponema pallidum</i> Nichols	tr p	Spirochaetales	+	1	+	abd		+	-	300	209	1.44	2.5E-05
<i>Tropheryma whipplei</i> TW08/27	to w	Actinobacteria	+	1	+	abd		-	-	286	235	1.22	0.012
<i>Ureaplasma urealyticum</i>	ur u	Firmicutes, Mollicutes	+	1	-	(abd)	shift of extreme; distance between boxes > 100 bp	+	-	315	264	1.20	0.016
<i>Vibrio cholerae</i> O1 N16961 chr. I	vi c	γ Proteobacteria	+	1	+	abd		+	+	1044	707	1.48	4.2E-16
<i>Vibrio cholerae</i> O1 N16961 chr. II	vi c	γ Proteobacteria	+	0	+	O		-	-	370	265	1.40	1.6E-05
<i>Vibrio parahaemolyticus</i> RIMD2210633 chr. I	vi p	γ Proteobacteria	+	1	+	abd		-	-	928	867	1.07	0.073
<i>Vibrio parahaemolyticus</i> RIMD2210633 chr. II	vi p	γ Proteobacteria	+	0	+	O		-	-	528	495	1.07	0.154
<i>Vibrio vulnificus</i> CMCP6 chr. I	vi v	γ Proteobacteria	+	1	+	abd		-	+	968	828	1.17	4.7E-04
<i>Vibrio vulnificus</i> CMCP6 chr. II	vi v	γ Proteobacteria	+	0	+	O		-	-	527	452	1.17	0.008
<i>Wigglesworthia glossinidia</i>	wi g	γ Proteobacteria	+	0	-	O		-	-	194	230	0.85	0.042
<i>Wolbachia pipientis</i> wMel	wl p	α Proteobacteria	-	1	+	O		-	-	463	441	1.05	0.2275
<i>Wolinella succinogenes</i>	wo s	ε Proteobacteria	+	1	-	ad		-	-	569	487	1.17	0.006
<i>Xanthomonas axonopodis</i> pv. citri 306	xa a	γ Proteobacteria	+	1	+	(a)bd	shift of extreme	-	+	320	371	0.86	0.026
<i>Xanthomonas campestris</i> ATCC33913	xa c	γ Proteobacteria	+	1	+	(abd)	two boxes; shift of extreme	-	-	328	353	0.93	0.168
<i>Xylella fastidiosa</i> 9a5c	xy f	γ Proteobacteria	+	1	+	abd		-	-	608	495	1.23	3.2E-04
<i>Yersinia pestis</i> CO92	ye p	γ Proteobacteria	+	1	+	abd		+	-	1853	1115	1.66	3.6E-42

abbr. – abbreviation of bacteria name; A – presence of clear DNA asymmetry with two global extrema seen in the DNA walk; *dnaA* – number of *dnaA* genes in the genome; C – presence of at least one cluster of three DnaA boxes with average distance between them less than 100 bp; co-loc. – co-localisation of putative *oriC* by three methods (a – method of DNA asymmetry; b - DnaA boxes' distribution; d - *dnaA* gene location); G – presence of at least three separated clusters of DnaA boxes seen in the global scale (with the distances to the *oriC* region up to 800 kb); L - presence of groups of clusters in local scale seen, at least two separate clusters of DnaA boxes in the distances between them up to 7 kb; obs. – number of observed DnaA boxes; exp. – number of expected DnaA boxes counted from the base composition of the given genome; obs/exp - ratio between the above numbers of boxes; *p* – *p* value in the *t*-test; significance of the difference between obs. and exp.; term *shift* in the 'note' column means that the sites indicated by different methods are in the distance greater than 1% and less than 7% of the chromosome length.